

# Figure 11. Homology of *Drosophila how* (GadFly Accession Number CG10293) to human Quaking isoforms

## Figure 11A. BLASTP results for CG10293 (GadFly Accession Number)

gb|AAF63416.1|AF142421\_1 (AF142421) QUAKING isoform 5 [Homo sapiens]  
Length = 337

Score = 289 bits (739), Expect = 5e-77  
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)  
Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 24

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240  
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357  
P A P PLI + V + PTAA G G+I+ PY+Y Y  
Sbjct: 240 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 292

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389  
+L + S +GA+ + R R HPYQR  
Sbjct: 293 ATSILEYPIEPSGVLGAVATKVRRHDMRVHPYQR 326

ref|XP\_037438.2| (XM\_037438) similar to KH domain RNA binding protein QKI-5A  
[Homo sapiens], Length = 341

Score = 289 bits (739), Expect = 5e-77  
Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)  
Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 25

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240  
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357  
 P A P PLI + V + + PTAA G G+I+ PY+Y Y  
 Sbjct: 244 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 296

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389  
 +L + S +GA+ + R R HPYQR  
 Sbjct: 297 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 330

gb|AAF63414.1|AF142419\_1 (AF142419) QUAKING isoform 6 [Homo sapiens]  
 Length = 363

Score = 289 bits (739), Expect = 5e-77  
 Identities = 168/334 (50%), Positives = 215/334 (64%), Gaps = 20/334 (5%)  
 Query: SEQ ID NO: 23; Sbjct: SEQ ID NO: 26

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120  
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
 Sbjct: 88 EKRSaelPDavgPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHLVITVEDTENRATVKLAQAVAEVQKLLVPQAE 240  
 KGSMRDKKKE+ NRGKPNWEHL++DLHLVITVED +NRA +KL +AV EV+KLLVP AEG  
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDLHLVITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 265

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALA 357  
 P A P PLI + V + + PTAA G G+I+ PY+Y Y  
 Sbjct: 266 PTPAGPTIMPLIRQIQTA-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAP 318

Query: 358 GNPLLTEYADHS--VGAIKQORRLATNREHPYQR 389  
 +L + S +GA+ + R R HPYQR  
 Sbjct: 319 ATSILEYPIEPSGVLGAVATKVRHRDMRVHPYQR 352

dbj|BAB55032.1| (AK027309) unnamed protein product [Homo sapiens]  
 Length = 323

Score = 282 bits (722), Expect = 5e-75  
 Identities = 165/320 (51%), Positives = 208/320 (64%), Gaps = 20/320 (6%)  
 Query: SEQ ID NO: 27; Sbjct: SEQ ID NO: 28

Query: 81 QLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-VKKEPLTLPEPEGSV 134  
 QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+ G +  
 Sbjct: 2 QLMNDKKLMSSLPNFCGIFNHLERLLDEEISVRKDMYNDTLNGSTEKRSaelPDavgPI 61

Query: 135 VTMNEKVYPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKEDANR 194  
 V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE+ NR  
 Sbjct: 62 VQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRGKGSMRDKKKEQNR 121

Query: 195 GKPNWEHLSDDLHLVITVEDTENRATVKLAQAVAEVQKLLVPQAEGEDELKKRQLMELAI 254  
 GKPNWEHL++DLHLVITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLMELAI  
 Sbjct: 122 GKPNWEHLNEDLHLVITVEDAQNRAEIKLKRAVEEVKLLVPAAEGEDSLKKMQLMELAI 181

Query: 255 INGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAPLILN 313  
 +NGTYRD KS A+ A + R++T A +R P A P PLI  
 Sbjct: 182 LNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRTPTPAGPTIMPLIRQ 239

Query: 314 PRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDYANYAALAGNPLLTEYADHS-- 369  
 + V + + PTAA G G+I+ PY+Y Y +L + S  
 Sbjct: 240 IQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIEPSGV 292

Query: 370 VGAIKQQRRLATNREHPYQR 389  
 +GA+ + R R HPYQR  
 Sbjct: 293 LGAVATKVRRHDMRVHPYQR 312

gb|AAF63413.1|AF142418\_1 (AF142418) QUAKING isoform 2 [Homo sapiens]  
 Length = 347

Score = 280 bits (716), Expect = 2e-74  
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 30

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120  
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
 Sbjct: 88 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240  
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAILNGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAPALRT 265

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
 P A P PLI + V + + PTAA G G+I+ PY+Y  
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63417.1|AF142422\_1 (AF142422) QUAKING isoform 3 [Homo sapiens]  
 Length = 341

Score = 280 bits (716), Expect = 2e-74  
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 31

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120  
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
 Sbjct: 28 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVKMDMYNDTLNGST 87

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
 Sbjct: 88 EKRSaelPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 147

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQVQKLLVPQAEG 240  
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
 Sbjct: 148 KGSMRDKKKEEQNRGKPNWEHLNEDDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 207

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300  
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
 Sbjct: 208 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 265

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
 P A P PLI + V + + PTAA G G+I+ PY+Y  
 Sbjct: 266 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 312

gb|AAF63415.1|AF142420\_1 (AF142420) QUAKING isoform 4 [Homo sapiens]  
 Length = 315

Score = 280 bits (716), Expect = 2e-74  
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 32

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
 Sbjct: 2 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
 Sbjct: 62 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240  
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
 Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300  
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
 Sbjct: 182 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 239

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
 P A P PLI + V + + PTAA G G+I+ PY+Y  
 Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BAB69497.1| (AB067799) RNA binding protein HQK-6 [Homo sapiens]  
 Length = 319

Score = 280 bits (716), Expect = 2e-74  
 Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
 Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 33

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
 + ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
 Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
 +K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
 Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAEOVKLLVPQAEG 240  
 KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
 Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAEG 185

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRRRLVAASDSRLLTSTGLPGLAAQIRA 300  
 ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
 Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPPAALRT 243

22/51

Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
P A P PLI + V + + PTAA G G+I+ PY+Y  
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69499.1| (AB067801) RNA binding protein HQK-7B [Homo sapiens]  
Length = 319

Score = 280 bits (716), Expect = 2e-74  
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 34  
Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65  
Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125  
Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEG 240  
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAG 185  
Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243  
Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
P A P PLI + V + + PTAA G G+I+ PY+Y  
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

dbj|BAB69498.1| (AB067800) RNA binding protein HQK-7 [Homo sapiens]  
Length = 325

Score = 280 bits (716), Expect = 2e-74  
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 35  
Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIARVRASLFQ--ING-V 120  
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
Sbjct: 6 ETKEKPKPTPDYLMQLMNDKKLMSSLPNFCGIFNHLERLLDEEISRVRKDMYNDTLNGST 65  
Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
Sbjct: 66 EKRSAELPDAVGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEAETGCKIMVRG 125  
Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAQKLLVPPQAEG 240  
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
Sbjct: 126 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRAEIKLKRAVEEVKLLVPAAG 185  
Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
Sbjct: 186 EDSLKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPAAALRT 243  
Query: 301 PA-AAPLGAPLIILNPRMTVPTTAASILSAQAAPTAAFDQTG--HGMIFAPYDY 350  
P A P PLI + V + + PTAA G G+I+ PY+Y  
Sbjct: 244 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 290

gb|AAF63412.1|AF142417\_1 (AF142417) QUAKING isoform 1 [Homo sapiens]  
Length = 321

Score = 280 bits (716), Expect = 2e-74  
Identities = 156/293 (53%), Positives = 198/293 (67%), Gaps = 17/293 (5%)  
Query: SEQ ID NO: 29; Sbjct: SEQ ID NO: 36

Query: 67 QQQQSTQSIADYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-V 120  
+ ++ + DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG  
Sbjct: 2 ETKEKPKPTPDYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISRVKDMYNDTLNGST 61

Query: 121 KKEPLTLPEPEGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRG 180  
+K LP+ G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRG  
Sbjct: 62 EKRSaelPDavgPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEaETGCKIMVRG 121

Query: 181 KGSMRDKKKEDANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAevQKLLVPQAEG 240  
KGSMRDKKKE+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEG  
Sbjct: 122 KGSMRDKKKEEQNRGKPNWEHLNEDLHVLITVEDAQNRaeIKLKRAVEEVKLLVPAAEG 181

Query: 241 EDELKKRQLMELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRA 300  
ED LKK QLMELAI+NGTYRD KS A+ A + R++T A +R  
Sbjct: 182 EDslKKMQLMELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPpAALRT 239

Query: 301 PA-AAPLGAPLILNPRMTVPTTAASILSAQAAPTAafdQTG--HGMIFAPYDY 350  
P A P PLI + V + + PTAA G G+I+ PY+Y  
Sbjct: 240 PTPAGPTIMPLIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEY 286

dbj|BD004960.1| Genes related to stomach cancer, Length = 1993

Score = 288 bits (738), Expect = 1e-77  
Identities = 168/324 (51%), Positives = 211/324 (64%), Gaps = 11/324 (3%)  
Frame = +1  
Query: SEQ ID NO: 37; Sbjct: SEQ ID NO: 38

Query: 77 DYLAQLLKDRKQLAAFPN---VFTHVERLLDEEIIARVRASLFQ--ING-VKKEPLTLPEP 130  
DYL QL+ D+K +++ PN +F H+ERLLDEEI+RVR ++ +NG +K LP+  
Sbjct: 4 DYLMQLMNDKMLSSLPNFCGIFNHLERLLDEEISRVKDMYNDTLNGSTeKRSaelPDA 183

Query: 131 EGSVVTMNEKVYVPVREHPDFNFVGRILGPRGMTAKQLEQETGCKIMVRGKGSMRDKKKE 190  
G +V + EK+YVPV+E+PDFNFVGRILGPRG+TAKQLE ETGCKIMVRGKGSMRDKKKE  
Sbjct: 184 VGPIVQLQEKLYVPVKEYPDFNFVGRILGPRGLTAKQLEaETGCKIMVRGKGSMRDKKKE 363

Query: 191 DANRGKPNWEHLSDDLHVLITVEDTENRATVKLAQAVAevQKLLVPQAEGEDELKKRQLM 250  
+ NRGKPNWEHL++DLHVLITVED +NRA +KL +AV EV+KLLVP AEGED LKK QLM  
Sbjct: 364 EQNRGKPNWEHLNEDLHVLITVEDAQNRaeIKLKRAVEEVKLLVPAAEGEDSLKKMQLM 543

Query: 251 ELAIINGTYRDTTAKSVAVCDEEWRLVAASDSRLLTSTGLPGLAAQIRAPA-AAPLGAP 309  
ELAI+NGTYRD KS A+ A + R++T A +R P A P P  
Sbjct: 544 ELAILNGTYRDANIKSPALAFS--LAATAQAAPRIITGPAPVLPpAALRTPTPAGPTIMP 717

Query: 310 LILNPRMTVPTTAASILSAQAAPTAafdQTG--HGMIFAPYDYANYAALAGNPLLTEYAD 367  
LI + V + + PTAA G G+I+ PY+Y Y +L +  
Sbjct: 718 LIRQIQTAV-----MPNGTPHPTAAIVPPGPEAGLIYTPYEYP-YTLAPATSILEYPIE 876

Query: 368 HS--VGAIKQQRRLATNREHPYQR 389  
S +GA+ + R R HPYQR  
Sbjct: 877 PSGVLGAVATKVRRHDMRVHPYQR

**Figure 15. Homology of Drosopila GadFly Accession Number CG9373 to human KIAA1443 protein, human unnamed protein product, and human myelin gene expression factor 2**

**Figure 15A. BLASTP results for GadFly Accession Number CG9373 Homology to human protein BAA92579.1 (GenBank Accession Number)**

dbj|BAA92579.1| (AB037762) KIAA1341 protein [Homo sapiens], Length = 620

Score = 249 bits (635), Expect = 1e-64

Identities = 207/660 (31%), Positives = 295/660 (44%), Gaps = 148/660 (22%)

Query: SEQ ID NO: 44; Sbjct: SEQ ID NO: 45

Query: 1 MSMDASNSVESREKERDRRGRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58  
+ M+ S + + + + G++ +RF + N G G + G RN R

Sbjct: 72 VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 121

Query: 59 VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESCKARGCGIVEFKDPENVQKALEKM 118  
V+ISNIPYD+WQ+KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M

Sbjct: 122 VFISNIPYDMKWQAIDLMREKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 181

Query: 119 NRYEVNGRELVVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNNGGGGGGGGGRDHMD 178  
N+Y+++GR L +KED + + + R GG GG H+

Sbjct: 182 NKYDLSGRPLNIKEDPDGENARRA-LQRTGGSFPGG-----HVP 219

Query: 179 DRDRGFSSRDDRRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVAN 238  
D G L NN N+ +N +G L + +FVAN

Sbjct: 220 DMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVAN 259

Query: 239 LDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISM LDRQMLF 298  
LD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q LF

Sbjct: 260 LDFKVGWKKLKEVFSIAGTVKRAIDKDKGSRGMGTVTTFEQAIEAVQAISMFGNQFLF 319

Query: 299 DRRTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPPNGGQSQ 350  
DR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+

Sbjct: 320 DRPMHVKMDDKSVPHYYRSHDGKTPQLPRGLGGIGMGLGPGGQPISASQLNI----- 372

Query: 351 GQLLGNAQQGSQLGSGVGSQPNSSAVSNATTNLLNNLTGVMFGNHAHVQPSVPAPVQKPSL 410  
G ++GN G + G FG +

Sbjct: 373 GGVMGNLGPFGM-----GMDGPGFGG-----MNRI 397

Query: 411 GNNTGSGGLNLLNLPNSILAAVVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGNS 462  
G G GGL N +G G G G L ++SS+ ++G+N G

Sbjct: 398 GGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRGFG 449

Query: 463 GNDDNLPPSNVGLSNNYSSGGTGGGNSYSSGNNYSGGGGSSN-----LGYNAYSSS-G 514  
+ L + +G +G G N G+ SGG GS N +G+ SSS

Sbjct: 450 DSFGRLGSAMIG----GFAGRIGSSNMGPVSGISGGMGSMNSVTGGMGMLDRMSSSFD 505

Query: 515 GMGGGNGGVGVDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTIIIKNVPIITC 574  
MG G G + D + G G G +GS K + I ++N+P

Sbjct: 506 RMGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDL 554

Query: 575 TWQTLRDKFRIGDVKFAEI-----RGNDVGVRFFKERDAELALALMDGSRLDGRNIKV 629  
TWQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V

Sbjct: 555 TWQKLKEKFSQCCHVMPAEIKMENGKSKGCGTVRFDSPEAEKACRIMNGIKISGREIDV 614

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 47

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79  
G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +  
Sbjct: 510 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 565

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELVVKED 133  
G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D  
Sbjct: 566 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLD 617

Score = 56.2 bits (134), Expect = 1e-06

Identities = 46/180 (25%), Positives = 76/180 (41%), Gaps = 21/180 (11%)

Query: SEQ ID NO: 48; Sbjct: SEQ ID NO: 49

Query: 139 DQYGRIVRDGGGGGGG-----GGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRD 188  
D +GR+ GG G G G+ GG G N GG G +D F R  
Sbjct: 450 DSFGRLGSAMIGGFAGRIGSSNMGPVGSIGSGMGSMSVGTGGMGMG-LDRMSSSFDRM- 507

Query: 189 DDRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKL 248  
G ++ + + + + E +G G N++FV NL + + +KL  
Sbjct: 508 -----GPGIGAILERSIDMDRGFLSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKL 559

Query: 249 KQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308  
K+ F G V ++ ++ G S+G + +D P A +A +++ + R + VRLDR  
Sbjct: 560 KEKFSQCGHVMFAEIKMEN-GKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDR 618

### Homology to human protein BAB14421.1 (GenBank Accession Number)

>dbj|BAB14421.1| (AK023133) unnamed protein product [Homo sapiens],  
Length = 576

Score = 242 bits (618), Expect = 1e-62

Identities = 206/654 (31%), Positives = 289/654 (43%), Gaps = 160/654 (24%)

Query: SEQ ID NO: 44; Sbjct: SEQ ID NO: 50

Query: 1 MSMDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCR 58  
+ M+ S + + + + G++ +RF + N G G + G RN R  
Sbjct: 52 VKMENDESAKEEKSDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-R 101

Query: 59 VYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKM 118  
V+ISNIPYD +WQ +KDL R VG + YV+LF D GK+RGCG+VEFKD E V+KALE M  
Sbjct: 102 VFISNIPYDMKWQAIKDLMEKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKKALETM 161

Query: 119 NRYEVNGRELVVKED-HGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDH 177  
N+Y+++GR L +KED GE + + R GG GG H+  
Sbjct: 162 NKYDLSGRPLNIKEDPDGENARRASQ--RTGGSFPGG-----HV 198

Query: 178 DDRDRGFSRRDDRLSGRNNFNMMSSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA 237  
D G L NN N+ +N +G L + +FVA  
Sbjct: 199 PDMGSGLMNLPPSIL---NNPNIPPEVISNLQ-----AGRLGSTIFVA 238

Query: 238 NLDYKVDNKKLKQVFKLAGKVQSVDSLSDKEGNSRGFAVIEYDHPVEAVQAISMLDRQML 297  
NLD+KV KKLK+VF +AG V+ D+ DK+G SRG + ++ +EAVQAISM + Q L  
Sbjct: 239 NLDKFKVGWKKLKEVFSIAGTVKRADIKEDKDGKSRGMGTVTFEQAIEAVQAISMFGQFL 298

Query: 298 FDRRMTVRLD--RIPDK-----NEGIKLPEGLGGVGIGLGPNGEPLRDVAHNLPNGGQS 349



Sbjct: 299 FDR M V++D +P + + +LP GLGG+G+GLGP G+P+ N+  
 Query: 350 QGQLLGNAQQGSQGLSVGSQPNSSAVSNATTNLLNNLTGVMFGNHAAVQSPVAPVQKPS 409  
 G ++GN G + G FG  
 Sbjct: 353 -GGVMGNLGP GGM-----GMDGPGFGG-----MNR 376  
 Query: 410 LGNNTGSGGLNLLNNLNP SILAAVGNLGNQG--GNLSNPLLSSSL-----SNLGLNLGN 461  
 +G G GGL N +G G G G L ++SS+ ++G+N G  
 Sbjct: 377 IGGGIGFGGLEAMN-----SMGGFGGVGRMGELYRGAMTSSMERDFGRGDIGINRG- 427  
 Query: 462 SGNDNLPSPSNVGLSNYSSGGTGGGNSYSSGNNYSGGGSSNLGYNAYSSS-GGMGGGN 520  
 G S GG GG NS + G +G + SSS MG G  
 Sbjct: 428 -----FGDSFGRLGGGMGGMNSVT-----GGMGMGLDRMSSSFDRMGPGI 467  
 Query: 521 GGVGVDGNDYNTGNPLDVYGGGNSVGSANAVGASRKSDTIIKKNVPITCTWQTLR 580  
 G + D + G G G +GS K + I ++N+P TWQ L+  
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLFPDLTWQKLK 516  
 Query: 581 DKFREIGDVKFAEI-----RGNDVGVRFFKERDAELAIALMDGSRRLDGRNIKV 629  
 +KF + G V FAEI + G VRF AE A +M+G ++ GR I V  
 Sbjct: 517 EKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDV 570

Score = 72.8 bits (177), Expect = 1e-11

Identities = 82/348 (23%), Positives = 133/348 (37%), Gaps = 96/348 (27%)

Query: SEQ ID NO: 51; Sbjct: SEQ ID NO: 52

Query: 54 RRNCRVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQK 113  
 R ++++N+ + W+ LK++F I G+++ + D+ GK+RG G V F+ +  
 Sbjct: 230 RLGSTIFVANLDFKVGWKKLKEVFS-IAGTVKRA DIKEDKD GKS RGMGTVTTFEQAI EAVQ 288  
 Query: 114 ALEKMNR YE VNGREL VVKED-----HGEQRDQYGRIVRDGGGGGGGG----- 155  
 A+ N + R + VK D H E R G+ + G GG G  
 Sbjct: 289 AISMFNGQFLFDRPMHV KMDDKSV PHEEYRSHD GKT PQLPRGLGGIGMGLGPGGQPISAS 348  
 Query: 156 ----GGVQG-----GNGGNNGGGGG-----GGRDHMDRDRDRGF 184  
 GGV G G GG N GGG GG M + RG  
 Sbjct: 349 QLNIGGV MGNLGP GGMGMDGPGFGGMNRIGGGIGFGGLEAMNSMGGFGGVGRMGELYRGA 408  
 Query: 185 SRRDDRLSGRNNFNMMSS-----NDYNNSSNYNLYGLSASFLES LG--- 225  
 +R GR + + N L +S+SF + +G  
 Sbjct: 409 MTSSMERDFGRGDIGINRGFGDSFGRLGGGMGGMNSVTGGMGMGLDRMSSSF-DRMGPGI 467  
 Query: 226 -----ISGPLH-----NKVFVANLDYKVDNKKLKQVFKLAGKVQS 260  
 +SGP+ N++FV NL + + +KLK+ F G V  
 Sbjct: 468 GAILERSIDMDRGFLSGPMGSGMRERIGSKGNQIFVRNLFPDLTWQKLKEKFSQCGHVMF 527  
 Query: 261 VDLSDKKEGNSRGFAVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308  
 ++ ++ G S+G + +D P A +A +++ + R + VRLDR  
 Sbjct: 528 AEIKMEN-GKSKGCGTVRFDSPESA EKACRIMNGIKISGREIDVRLDR 574

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 53

Query: 20 GRGARSRTDADGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79  
 G GA R D D G +G G G+ R+R + N ++++ N+P+D WQ LK+ F +  
 Sbjct: 466 GIGAILERSIDMD-RGFLSGPMGSGM---RERIGSKGN-QIFVRNLFPDLTWQKLKEKFSQ 521  
 Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNR YE VNGREL VVKED 133

G + + ++ E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D  
Sbjct: 522 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 573

### Homology to human protein NP057216.1 (GenBank Accession Number)

ref|NP\_057216.1| (NM\_016132) myelin gene expression factor 2 [Homo sapiens]  
gb|AAD43038.1| (AF106685) myelin gene expression factor 2 [Homo sapiens]  
Length = 547

Score = 238 bits (607), Expect = 2e-61  
Identities = 204/659 (30%), Positives = 295/659 (43%), Gaps = 150/659 (22%)  
Query: SEQ ID NO: 54; Sbjct: SEQ ID NO: 55

Query: 3 MDASNSVESREKERDRRGAR-GSRFTDADGNGN-GAGSQGGGVAARDRSRERRNCRVY 60  
M+ S + + + + G++ +RF + N G G + G RN RV+  
Sbjct: 1 MENDESAKEEKSDDLKEKSTGSKKANRFHPYSKDKNSGTGEKKG-----PNRN-RVF 50

Query: 61 ISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMN 120  
ISNIPYD +WQ +KDL R VG + YV+LF D GK+RCCG+VEFKD E V+KALE MN+  
Sbjct: 51 ISNIPYDMKWQAIKDLMREKVGEVTVYVELFKDAEGKSRGCGVVEFKDEEFVKALETMNK 110

Query: 121 YEVNGRELTVKEDHGEQRDQYGRIVRDGGGGGGGGGGVQGGNGGNGGGGGGGGRDHMD 180  
Y+++GR + +KED + + + R G QG + + G G  
Sbjct: 111 YDLSGRRVNIKEDPDGENARRA-LQRTGTS-----FQGS HASDVGSG----- 151

Query: 181 DRGFSRRDDRLSGRNNFMMSNDYMNSSNYNLYGLSASFLES LGISGPLHNKVFVANLD 240  
N+ + NN + + + +L +G L + +FVANLD  
Sbjct: 152 -----LVNLPPSILNNPN-----IPPEVISNLQ-AGRLGSTIFVANLD 188

Query: 241 YKVDNKKLKQVFKLAGKVQSVDSL DKEGNSRGFAVIEYDHPVEAVQAI SMLDRQMLFDR 300  
+KV KKLK+VF +AG V++ DK+G SRG + ++ +EAVQAISM + Q LFDR  
Sbjct: 189 FKGWKKLKEVFSIAGTVKAGSYKEDKD GKS RGMGTVTTFEQAI EAVQAISM FNGQFLFDR 248

Query: 301 RMTVRLD-----RIPDKNEG IKLPEGLGGVGIGLGPNGEPLRDVAHNL PNGGQS QG 351  
M V++D R PD + +LP GLGG+G+GLGP G+P+ N+ G  
Sbjct: 249 PMHVKMDDKSVPHEEYRSPD-GKTPQLPRGLGGIGMGLPGGPQIPISASQLNI-----G 300

Query: 352 QLLGNAQQGSQ LGSVGSQPNSSAVSNATTNLLNNLTGVMFGNHA AVQPSPVAPVQKPSLG 411  
++GN G + G FG +G  
Sbjct: 301 GVMGNLGP GGM-----GMDGPGFGG-----MNRIG 325

Query: 412 NNTGSGGLN LNNLNPSILAAVVG NLGNQG--GNLSNPLLSSSL S-----NLGLNLGNSG 463  
G GGL N +G G G G L ++SS+ ++GL+ G  
Sbjct: 326 GGIGFGGLEAMN-----SMGGFGGVGRMGEL YRGAMTSSMERDFGHRDIGLSRGFGD 377

Query: 464 NDDNLPPSNVGLSN NYSSGGTGGGNSYSSGN NYSSGGGGSSN-----LGYNAYSSS-GG 515  
+ L + +G +G G N G+ SGG GS N +G + SSS  
Sbjct: 378 SFGR LGSAMIG----GITGRIGSSNMGPVGS GISGGMGSMNSVTGGMGMGLDRMSSSFDR 433

Query: 516 MGGGNGGVGDGNDYNTGNPLDVYGGGNSVGNNSVGSANAVGASRKSDTII IKNVPITCT 575  
MG G G + D + G G G +GS K + I ++N+P T  
Sbjct: 434 MGPGIGAILERSIDMDRGFLSGPMGSGM---RERIGS-----KGNQIFVRNLPFDLT 482

Query: 576 WQTLRDKFREIGDVKFAEI-----RGNDVG VVRFFKERDAELALMDGSRLDGRNIKV 629  
WQ L++KF + G V FAEI + G VRF AE A +M+G ++ GR I V  
Sbjct: 483 WQKLKEKFSQCGHVMFAEIKMENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDV 541

Score = 68.6 bits (166), Expect = 2e-10

Identities = 41/114 (35%), Positives = 67/114 (57%), Gaps = 6/114 (5%)

Query: SEQ ID NO: 46; Sbjct: SEQ ID NO: 56

Query: 20 GRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNCRVYISNIPYDYRWQDLKDLFRR 79

G GA R D D G +G G G+ R+R + N +++ N+P+D WQ LK+ F +

Sbjct: 437 GIGAILERSIDMD-RGFLSGPMGSGM--RERIGSKGN-QIFVRNLPFDLTWQKLKEKFSQ 492

Query: 80 IVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEKMNRYEVNGRELIVVKED 133

G + + + + E+GK++GCG V F PE+ +KA MN +++GRE+ V+ D

Sbjct: 493 C-GHVMFAEIKM-ENGKSKGCGTVRFDSPESAEEKACRIMNGIKISGREIDVRLD 544

Score = 55.5 bits (132), Expect = 2e-06

Identities = 41/157 (26%), Positives = 69/157 (43%), Gaps = 11/157 (7%)

Query: SEQ ID NO: 57; Sbjct: SEQ ID NO: 58

Query: 152 GGGGGGVQGGNGGNGGGGGGGGRDHMDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNY 211

G G G+ GG G N GG G +D F R G ++ + +

Sbjct: 400 GPVGSGISGGMGSMNSVTGGMGMG-LDRMSSSFDRM-----GPGIGAILERSIDMDRGF 452

Query: 212 NLYGLSASFLESGLISGPLHNKVFVANLDYKVDNKKLKQVFKLAGKVQSVDLSDKEGNS 271

+ + E +G G N++FV NL + + +KLK+ F G V ++ ++ G S

Sbjct: 453 LSGPMGSGMRERIGSKG---NQIFVRNLPFDLTWQKLKEKFSQCGHVMFAEIKMEN-GKS 508

Query: 272 RGFVIEYDHPVEAVQAISMLDRQMLFDRRMTVRLDR 308

+G + +D P A +A +++ + R + VRLDR

Sbjct: 509 KCGCTVRFDSPESAEEKACRIMNGIKISGREIDVRLDR 545

### Figure 15B. Multiple Sequence Alignment (ClustalW 1.83)

CG9373 Dm -----  
KIAA1341 Hs PLSRSEPLSSGGRGGGSGGGMADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK  
MyEF-2 Hs -----  
FLJ13071 Hs -----MADANKAEVPGATGGDSPHLQPAEPPGEPRREPHPAEAEK

CG9373 Dm ---MSMDASNSVESREKERDRRGARGSRFTDADGNGNGAGSQGGGVAARDRSRERRNC  
KIAA1341 Hs QQPQHSSSSNGVKMENDESAAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN  
MyEF-2 Hs -----MENDESAAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN  
FLJ13071 Hs QQPQHSSSSNGVKMENDESAAKEEKS DLKEKSTGSKKANRFHPYSKDKNSGTGEKKGPNNRN

CG9373 Dm RYVYISNIPYDYRWQDLKDLFRRIVGSIEYVQLFFDESGKARGCGIVEFKDPENVQKALEK  
KIAA1341 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET  
MyEF-2 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET  
FLJ13071 Hs RVFISNIPYDMKWQA IKDLMREKVG EYTYVELFKDAEGKSRGCGVVEFKDEEFVKKALET

CG9373 Dm MNRYEVNGRELIVVKEDHGEQRDQYGRIVRDGGGGGGGGGGGVQGGNGGNGGGGGGGGRDHM  
KIAA1341 Hs MNKYDLSGRPLNIKEDPDGENARR-----ALQRTGGSFPGGHVPDMGSG-----  
MyEF-2 Hs MNKYDLSGRRVNIKEDPDGENARR-----ALQRTGTSFQGS HASDVGSG-----  
FLJ13071 Hs MNKYDLSGRPLNIKEDPDGENARR-----ASQRTGGSFPGGHVPDMGSG-----

CG9373 Dm DDDRDRGFSRRDDRLSGRNNFNMMNSNDYNNSSNYNLYGLSASFLESGLISGPLHNKVFVA  
KIAA1341 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA  
MyEF-2 Hs -----LVNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA  
FLJ13071 Hs -----LMNLPPSILNPNIPPEVISNLQ----AGRLGSTIFVA